SEQUENCE LISTING

<110> Nakamura, Yusuke
      Furukawa, Yoichi
      Oncotherapy Science, Inc.

<120> Method for Diagnosing Colorectal Cancers

<130> 082368-008900US

<140> US 10/589,594
<141> 2006-08-15

<150> WO PCT/JP04/02145
<151> 2004-02-24

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tcaagaccgt tgtctcttcg atcgcttctt tggacttggc gaccatttca gag atg 296
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tct tcc aga agt acc aaa gat tta att aaa agt aag tgg gga tcg aag   344
Ser Ser Arg Ser Thr Lys Asp Leu Ile Lys Ser Lys Trp Gly Ser Lys
            5   10   15

cct agt aac tcc aaa tcc gaa act aca tta gaa aaa tta aag gga gaa   392
Pro Ser Asn Ser Lys Ser Glu Thr Thr Leu Glu Lys Leu Lys Gly Glu
            20   25   30

att gca cac tta aag aca tca gtg gat gaa atc aca agt ggg aaa gga   440
Ile Ala His Leu Lys Thr Ser Val Asp Glu Ile Thr Ser Gly Lys Gly
        35   40   45

aag ctg act gat aaa gag aga cac aga ctt ttg gag aaa att cga gtc   488
Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg Val
    50   55   60   65

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ctt gag gct gag aag gag aag aat gct tat caa ctc aca gag aag gac     536
Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys Asp
                70                  75                  80

aaa gaa ata cag cga ctg aga gac caa ctg aag gcc aga tat agt act     584
Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser Thr
                    85                  90                  95

acc gca ttg ctt gaa cag ctg gaa gag aca acg aga gaa gga gaa agg     632
Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu Arg
            100                 105                 110

agg gag cag gtg ttg aaa gcc tta tct gaa gag aaa gac gta ttg aaa     680
Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu Lys
        115                 120                 125

caa cag ttg tct gct gca acc tca cga att gct gaa ctt gaa agc aaa     728
Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser Lys
130                 135                 140                 145

acc aat aca ctc cgt tta tca cag act gtg gct cca aac tgc ttc aac     776
Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe Asn
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tca tca ata aat aat att cat gaa atg gaa ata cag ctg aaa gat gct     824
Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp Ala
                165                 170                 175

ctg gag aaa aat cag cag tgg ctc gtg tat gat cag cag cgg gaa gtc     872
Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu Val
            180                 185                 190

tat gta aaa gga ctt tta gca aag atc ttt gag ttg gaa aag aaa acg     920
Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys Thr
        195                 200                 205

gaa aca gct gct cat tca ctc cca cag cag aca aaa aag cct gaa tca     968
Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu Ser
210                 215                 220                 225

gaa ggt tat ctt caa gaa gag aag cag aaa tgt tac aac gat ctc ttg    1016
Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu Leu
                230                 235                 240

gca agt gca aaa aaa gat ctt gag gtt gaa cga caa acc ata act cag    1064
Ala Ser Ala Lys Lys Asp Leu Glu Val Glu Arg Gln Thr Ile Thr Gln
            245                 250                 255

ctg agt ttt gaa ctg agt gaa ttt cga aga aaa tat gaa gaa acc caa    1112
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aaa gaa gtt cac aat tta aat cag ctg ttg tat tca caa aga agg gca    1160
Lys Glu Val His Asn Leu Asn Gln Leu Leu Tyr Ser Gln Arg Arg Ala
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gat gtg caa cat ctg gaa gat gat agg cat aaa aca gag aag ata caa    1208
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aag aag aga tcc gaa gag ctc tta tct cag gtc cag ttt ctt tac aca   1304
Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr Thr
            325             330             335

tct ctg cta aag cag caa gaa gaa caa aca agg gta gct ctg ttg gaa   1352
Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu Glu
            340             345             350

caa cag atg cag gca tgt act tta gac ttt gaa aat gaa aaa ctc gac   1400
Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu Asp
        355             360             365

cgt caa cat gtg cag cat caa ttg cat gta att ctt aag gag ctc cga   1448
Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu Arg
370             375             380             385

aaa gca aga aat caa ata aca cag ttg gaa tcc ttg aaa cag ctt cat   1496
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gag ttt gcc atc aca gag cca tta gtc act ttc caa gga gag act gaa   1544
Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr Glu
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aac aga gaa aaa gtt gcc gcc tca cca aaa agt ccc act gct gca ctc   1592
Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala Leu
            420             425             430

aat gaa agc ctg gtg gaa tgt ccc aag tgc aat ata cag tat cca gcc   1640
Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro Ala
            435             440             445

act gag cat cgc gat ctg ctt gtc cat gtg gaa tac tgt tca aag tag   1688
Thr Glu His Arg Asp Leu Leu Val His Val Glu Tyr Cys Ser Lys
450             455             460

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            35                  40                  45
Gly Lys Leu Thr Asp Lys Glu Arg His Arg Leu Leu Glu Lys Ile Arg
        50                  55                  60
Val Leu Glu Ala Glu Lys Glu Lys Asn Ala Tyr Gln Leu Thr Glu Lys
65                  70                  75                  80
Asp Lys Glu Ile Gln Arg Leu Arg Asp Gln Leu Lys Ala Arg Tyr Ser
                85                  90                  95
Thr Thr Ala Leu Leu Glu Gln Leu Glu Glu Thr Thr Arg Glu Gly Glu
            100                 105                 110
Arg Arg Glu Gln Val Leu Lys Ala Leu Ser Glu Glu Lys Asp Val Leu
            115                 120                 125
Lys Gln Gln Leu Ser Ala Ala Thr Ser Arg Ile Ala Glu Leu Glu Ser
    130                 135                 140
Lys Thr Asn Thr Leu Arg Leu Ser Gln Thr Val Ala Pro Asn Cys Phe
145                 150                 155                 160
Asn Ser Ser Ile Asn Asn Ile His Glu Met Glu Ile Gln Leu Lys Asp
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Ala Leu Glu Lys Asn Gln Gln Trp Leu Val Tyr Asp Gln Gln Arg Glu
            180                 185                 190
Val Tyr Val Lys Gly Leu Leu Ala Lys Ile Phe Glu Leu Glu Lys Lys
            195                 200                 205
Thr Glu Thr Ala Ala His Ser Leu Pro Gln Gln Thr Lys Lys Pro Glu
    210                 215                 220
Ser Glu Gly Tyr Leu Gln Glu Glu Lys Gln Lys Cys Tyr Asn Asp Leu
225                 230                 235                 240
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                245                 250                 255
Gln Leu Ser Phe Glu Leu Ser Glu Phe Arg Arg Lys Tyr Glu Glu Thr
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            275                 280                 285
Ala Asp Val Gln His Leu Glu Asp Asp Arg His Lys Thr Glu Lys Ile
    290                 295                 300
Gln Lys Leu Arg Glu Glu Asn Asp Ile Ala Arg Gly Lys Leu Glu Glu
305                 310                 315                 320
Glu Lys Lys Arg Ser Glu Glu Leu Leu Ser Gln Val Gln Phe Leu Tyr
            325                 330                 335
Thr Ser Leu Leu Lys Gln Gln Glu Glu Gln Thr Arg Val Ala Leu Leu
            340                 345                 350
Glu Gln Gln Met Gln Ala Cys Thr Leu Asp Phe Glu Asn Glu Lys Leu
            355                 360                 365
Asp Arg Gln His Val Gln His Gln Leu His Val Ile Leu Lys Glu Leu
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Arg Lys Ala Arg Asn Gln Ile Thr Gln Leu Glu Ser Leu Lys Gln Leu
385                 390                 395                 400
His Glu Phe Ala Ile Thr Glu Pro Leu Val Thr Phe Gln Gly Glu Thr
                405                 410                 415
Glu Asn Arg Glu Lys Val Ala Ala Ser Pro Lys Ser Pro Thr Ala Ala
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Leu Asn Glu Ser Leu Val Glu Cys Pro Lys Cys Asn Ile Gln Tyr Pro
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<210> 6
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<210> 9
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<210> 10
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<210> 11
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<210> 12
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<220>
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<210> 13
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<210> 14
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<210> 15
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<210> 16
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     (psiH1BX-C10orf3-G)

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<220>
<223> C10orf3 siRNA oligonucleotide target sequence

<400> 21
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<210> 22
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<212> DNA
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<220>
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<212> DNA
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      DNA fragment insertion site

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<212> DNA
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<220>
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